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S14871	S07923	EEWTA	T03454	T03455	S29521	T00377	D22364	C22364	S10015	B22364	JC4851	D82493	A26892	T29475	T14004
suppressor	alpha/beta-gliadi	alpha/beta-gliadi	ALR protein -	ALR protein -	casein kinase I ho	KIAA0642 protein	alpha/beta-gliadi	alpha/beta-gliadi	alpha/beta-gliadi	alpha/beta-gliadi	hypoxia-inducible	conserved hypothet	Mopa box protein	hypothetical	tria protein

## ALIGNMENTS

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alpha-globulin type B precursor (tandem 1) - upland cotton (fragment W;Alternate names: seed storage protein C;Species: Gossyptum hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-5 C;Accession: S08059 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 A;Title: Developmental biochemistry of cottonseed embryogenesis and
                                                                                                                                                                                                                     RESULT
S08059
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Thes 39; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
E;1-25/Domain: signal sequence #status predicted <SIG>
E;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
E;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-81 <CH2>
C; Comment: This is a seed storage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII A;Reference number: A30838
A;Accession: A30838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C;Specles: Gossyptum hirsutum (upland cotton) C;Date: 30-Sep-1991 #seguence_revision 30-Sep-1991 #text_change 16-Jul-1999 C;Accession: A30838; S06911
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A; Accession: S06911
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R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
R;Chlan, Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-588 <CHL>
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97.5%;
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Pred. No. 5e-16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                               30-Sep-1993
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     germination. XIX
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A; Reference number:

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A;Cross-references: EMBL:X62626
C;Genetics:
A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C;Superfamily: 9lycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predi
F;25-566/Product: vicilin #status predicted
                                                                                                                                                                                                                                                                      R;McHenry, L.; Fritz, p.J.

R;McHenry, L.; Fritz, p.J.

R;McHenry, L.; Fritz, p.J.

R;McHenry, L.; Fritz, p.J.

A;Title: Comparison of the structure and nucleotide sequence of vicilin genes of cocoa A;Reference number: S22477; MUID:92288309

A;Accession: S22477
                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-452 <MC2>
                                                                                                                                                                                                                                         A;Cross-references:
A;Accession: S22478
                                                                                                                                                                                                                                                                                                                                                                      C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A.Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                vicilin precursor - cacao
       Query Match
Best Local Similarity
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S06398
alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
N;Correct Gossypium hirsutum (upland cotton)
The correct Gossypium Alternate Tavision 31-Mar-1
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C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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A; Accession: S06398
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A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
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Best Local Similarity
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A:Status: not compared with conceptual translation
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38; Conser
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         52.9%;
45.0%;
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53.8%;
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*; Pred. No. 3e-15;

**:^*^matches 0;
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Pred. No. 8.4e-08;
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119; DB 2;
No. 2e-05;
                                                                          <MAT>
                                                                                      <SIG>
                Length 566;
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homeotic protein prospero - fruit fly (Drosophila melanogaster) (Species: Drosophila melanogaster) (C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change C:Accession: S24548; JQ1397; A41089
submitted to the EMBL Data A; Reference number: S24548
                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein A-IV - crab-eating macaque C;Species: Macaca fascicularis (crab-eating macaque) C;Date: 06-Jan-1955 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999 C;Accession: S30195, S29565 R;Osada, J.; Pocovi, M.; Nicolosi, R.J.; Schaefer, E.J.; Ordovas, J.M. Biochim. Biophys. Acta 1172, 335-339, 1993 A;Title: Nucleotide sequences of the Macaca fascicularis apolipoprotein C-I.
                                                                                                                                                                                                                                                                                                                                       A:Introns: 17/1
C:Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-429 <OSA>
                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X68361; NID:g38050; PIDN:CAA48421.1; PID:g38051
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S30195; MUID:93192330
A;Accession: S30195
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submitted to the EMBL Data Library, January 1995
A;Description: An MDR transporter/serine protease gene
A;Reference number: Z18850
A;Accession: T18267
                                                                                                                                                                                                                                                                       Query Match
Best Local
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18267
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A; Residues: 1-1905 <
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T18267
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                                                                                                                                                                                                                                                                    36.9%;
46.2%;
        Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.2%;
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                                                                                                                                                                                                                                                             Score 83; [
Pred. No. 0.
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                                                 20-Feb-1995 #text_change
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A;Title: Highly conserved core domain and unique N A;Reference number: S10944; MUID:90326195 A;Accession: S10944
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C:Keywords: DNA binding; nucleus; transcr
F:717-734/Region: glutamine-rich
F:991-998/Region: nuclear location signal
F:1029-1049/Region: glutamine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-75,'GQDAERAVWPPDEAGPGRNEWPA',99-119,'NLALQFHVQVAAAAAITTALLPPIG',145-676,
A;Cross-references: GB:M81389; NID:g158183; PID:g158184
                                                                                                                                                                                                                                                             A; MoLecule type: DNA
A; Residues: 1-17,'N',19-186,'R',188-339
R: Hoffmann, A.; Sinn, E.; Yamamoto, T.;
Nature 346, 387-390, 1990
                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Cloning of a transcriptionally active human A; Reference number: A34831; MUID:90302010 A; Accession: A34831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: GB:M55654; NID:g339491; PIDN:AAA36731.1; PID:g339492 R:Kao, C.C.; Lieberman, P.M.; Schmidt, M.C.; Zhou, Q.; Pei, R.; Berk, A. Science 248, 1646-1649, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Peterson, M.G.; Tanese, N.; Pugh, B.F.; Tjian, Science 248, 1625-1630, 1990
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A;Residues: 1-417,'Q',419-1403 <MAT>
A;Residues: 1-617,'Q',419-1403 <MAT>
A;Cross-references: GB:D10609; DDBJ:D90560; NID:g217345; PID:d1001939; PID:g217346
A;Crossin, H; Grell, E.; Wolff, E.; Bier, E.; Jan, L.Y.; Jan, Y.N.
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A:Molecule type: DNA
A:Residues: 1-1403 <DOE>
A:Residues: 1-1403 <DOE>
A:Cross-references: EMBL:Z11743; NID:g8383; PID:g8384
A:Cross-references: EMBL:Z11743; NID:g8383; PID:g8384
R:Matsuzaki, F.; Koizumi, K.; Hama, C.; Yoshioka, T.; Nabeshima, Y.
Biochem. Biophys. Res. Commun. 182, 1336-1332, 1992
A:Title: Cloning of the Drosophila prospero gene and its expression A; Reference number: JQ1397; MUID:92171948
A:Accession: JQ1397
          A; Title: Clu
A; Reference
                                                       A;Residues: 1-91,96-339 <HOF>
A;Cross-references: EMBL:X54993; NID:g37065;
R;Kao, C.; Lieberman, P.; Schmidt, M.; Zhou,
Science 248, 1626, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-339 < PET>
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                                                                                                                                                           A; Molecule type: mRNA
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Best Local Similarity 54.8
Matches 17; Conservative
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          of the human TATA binding factor: Expression er: I60128
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Pred. No.
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T.; Wang, J.;
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                            of a transcriptionally
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Query Match
Best Local Similarity
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R:Kuspa, A.; Lu, S.; Souza, G.M. submitted to the EMBL Data Library. Ja A; Description: Yaka, a protein kinase A; Reference number: Z18146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hixson, J.E.; Kammerer, C.M.; Mott, G.E.; Britten, M.L.; Birnbaum, S.; Powers, J. Biol. Chem. 268, 15667-15673, 1993
A;Title: Baboon apolipoprotein A-TV. Identification of Lys76-->Glu that distingui A:Reference number: A47141; MUID:93340170
A;Status: preliminary
A;Status: preliminary
                                                                                A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1457 <KUS>
                                                                                                                                                                                                                    C; Accession: R; Kuspa, A.;
                                                                                                                                                                                                                                         protein kinase YakA (EC 2.7.1.-) - slime mold (Dictyostelium discoideum) (Species: Dictyostelium discoideum C;Species: Dictyostelium discoideum C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1 C;Accession: T14577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein A-IV I isoform - baboon (fragment)
C;Species: Papio sp. (baboon)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
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A47141
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C:Superfamily: human transcription initiation:
C:Keywords: alternative splicing; DNA binding;
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  A;Gene: yak/
C;Keywords:
                                         A;Cross-references: EMBL:AF045453;C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: intestine A; Note: sequence extracted from NCBI backbone (NCBIN:136009, NCBIP:136010) C; Superfamily: apolipoprotein A-I
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A; Residues: 1-401 <HIX>
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16; Conser
  phosphoprotein; phosphotransferase;
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                                                         NID: g2854116; PID: g2854117; PIDN: AAC02554.1
                                                                                                                                                                                                  January 1998
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35.6%; 38.5%;

Score Pred.

NO.

DB 2; 0.49;

Length 1457

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A;Description: catalyzes the formation of peptidy1-serine-phosphate or peptidy1-threonin A;Note: important for cell type differentiation and fruiting body morphogenesis C;Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain; protein kina F;126-223/Region: glutamine-rich F;126-223/Region: glutamine-rich F;297-312/Region: glutamine-rich F;334-590/Domain: protein kinase homology <KIN> F;342-550/Region: protein kinase ATP-binding mottif F;365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted F;464,468/Binding site: magnesium (Asn, Asp) #status predicted
                                                             рЬ
                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Introns: 578/3
C:Complex: heterodimer with regulatory chain; active catalytic chain is released when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M38703
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Isolation of two genes encoding putative protein kinases regulated during Dict. A;Reference number: JQ1150; MUID:91323730
A;Accession: JQ1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Accession: JQ1150 R;Buerki, E; Anjard, C.; Scholder, J.C.; Reymond, C. Gene 102, 57-65, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold (Dictyostelium C;Species: Dictyostelium discoideum C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: PK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-648 <BUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 1 - African malaria mosquito (fragment) C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change.09-Se C;Accession: S27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H. submitted to the EMBL Data Library, June 1992
A;Description: Distinct families of site-specific retroposons occupy A;Reference number: S27770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-613 <BES>
                                                                                                                                        Matches
                                                                                                                                                           Query Match
Best Local
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S27770
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17; Conser
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37.5%;
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                                                                                                                              Score 78; DB
Pred. No. 0.4;
12; Mismatches
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Pred. No. 0
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                                                                                                                                                 DB 1;
0.4;
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0.39;
                                                182
                                                                                                                                                                    Length 648
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C;Accession: T13675
R;Bolshakov, V.; Borkova, D.; Minana, B.; Kafatos, submitted to the EMBL Data Library, September 1998
                                                                                                                      hypothetical protein EG0002.3 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000
   A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule
                                              A; Reference number: 217698
                                                                                                                                                                                               RESULT
T13675
                                 A; Accession: T13675
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A;Map position: 13R
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A;Residues: 1-758 <HUN>
A;Cross-references: GB:Z49705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YMR164c - yeast (Saccharomyces cerevisiae) W;Alternate names: hypothetical protein YM8520.13c C:Species: Saccharomyces cerevisiae C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number:
A;Accession: S54522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SGD: MSS11
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Best Local S
Matches 15
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C;Superfamily: gliadin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AC3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
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A; Residues: 1-425 <W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary; translated from GB/EMBL/DDBJ
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R; McMurray, A.
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Best Local Similarity

Matches 14; Conserva
                                                                                                                                                                                                                                                                     293
                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 PVQCVPQCQQQCQQQCVQTQPTQQCQPQCQQQCVQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Bowman, S.
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                                                             Sequencing
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Conservative 10
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ce: clone AC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S54609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain
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                                                           the distal X chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library, May 1995
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AB972
                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                             Score 77; DB 2;
Pred. No. 0.58;
13; Mismatches
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Pred. No. 0.36;
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                                                  of Drosophila melanogaster
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